```
1    CGCTGCTCCTGCCGGGTGATGGAAAACCCCAGCCCGGCCGCCGCCCTGGGCAAGGCCCTC   60
1                        M  E  N  P  S  P  A  A  A  L  G  K  A  L    20

61   TGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTCCATC   120
21   C  A  L  L  L  A  T  L  G  A  A  G  Q  P  L  G  G  E  S  I    40

121  TGTTCCGCCAGAGCCCTGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACG   180
41   C  S  A  R  A  L  A  K  Y  S  I  T  F  T  G  K  W  S  Q  T    60

181  GCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG   240
61   A  F  P  K  Q  Y  P  L  F  R  P  P  A  Q  W  S  S  L  L  G    80

241  GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTG   300
81   A  A  H  S  S  D  Y  S  M  W  R  K  N  Q  Y  V  S  N  G  L    100

301  CGCGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGG   360
101  R  D  F  A  E  R  G  E  A  W  A  L  M  K  E  I  E  A  A  G    120

361  GAGGCGCTGCAGAGCGTGCACGCGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGG   420
121  E  A  L  Q  S  V  H  A  V  F  S  A  P  A  V  P  S  G  T  G    140

421  CAGACGTCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGC   480
141  Q  T  S  A  E  L  E  V  Q  R  R  H  S  L  V  S  F  V  V  R    160

481  ATCGTGCCCAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGAC   540
161  I  V  P  S  P  D  W  F  V  G  V  D  S  L  D  L  C  D  G  D    180

541  CGTTGGCGGGAACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGC   600
181  R  W  R  E  Q  A  A  L  D  L  Y  P  Y  D  A  G  T  D  S  G    200

601  TTCACCTTCTCCTCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACG   660
201  F  T  F  S  S  P  N  F  A  T  I  P  Q  D  T  V  T  E  I  T    220

661  TCCTCCTCTCCCAGCCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCT   720
221  S  S  S  P  S  H  P  A  N  S  F  Y  Y  P  R  L  K  A  L  P    240

721  CCCATCGCCAGGGTGACACTGGTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCC   780
241  P  I  A  R  V  T  L  V  R  L  R  Q  S  P  R  A  F  I  P  P    260

781  GCCCCAGTCCTGCCCAGCAGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACG   840
261  A  P  V  L  P  S  R  D  N  E  I  V  D  S  A  S  V  P  E  T    280

841  CCGCTGGACTGCGAGGTCTCCCTGTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGG   900
281  P  L  D  C  E  V  S  L  W  S  S  W  G  L  C  G  G  H  C  G    300

901  AGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGC   960
301  R  L  G  T  K  S  R  T  R  Y  V  R  V  Q  P  A  N  N  G  S    320

961  CCCTGCCCCGAGCTCGAAGAAGAGGCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAG   1020
321  P  C  P  E  L  E  E  E  A  E  C  V  P  D  N  C  V  *          340

1021 AGCCCCGCAGCCCCTGGGGCCCCCCGGAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCT   1080
1081 CATGCTGCAGGCGGCCGAGGGCACA                                      1105
```

FIG.1

```
rFSP    151  PTGTGCVILKASIVQKRIIYFQDEGSLTKKLCEQDPTLDGVTDRPILD..  198
                          :    ..:.|.| ||.   .  |..:.|: :
NAF-1     1  ..................MENPSPAAALGKALCALLLATLGAAGQPLGGES   33

rFSP    199  .CCACGTAKYRLTFYGNWSEKTHPKDYP..RRANHWSAIIGGSHSKNYVL  245
              |:| : |||.:|| |.||:.. ||:|| |.:.:||.::|:.||.:| :
NAF-1    34  ICSARALAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSM   83

rFSP    246  WEYGGYASEGVKQVAELGSPVKMEEEIRQQSDEVLTVIKAKAQWPSWQPV  295
              |  ..|.|:|:::.|| |.:  : .|| ..::.: .|   .| :.. ...
NAF-1    84  WRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSV...HAVFSAPAVP  130

rFSP    296  NVRAAPSAEFSVDRTRHLMSFLTMMGPSPDWNVGLSAESLCTKECGWVQK  345
              .. :..|||:.|:| : |:||:..:.|||| ||:.. |||. :  : |
NAF-1   131  SGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQA  180

rFSP    346  VVQDLIPWDAGTDSGVTYESPNKPTIPQEKIRPLT..SLDHPQSPFYDPE  393
              .: ||.|:|||||.|.|:.||| :|||:.: .:|  | .||...|| |
NAF-1   181  AL.DLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPR  229

rFSP    394  GGSITQVARVVIERIARKGEQCNIVPDNVDDIVADLAPEEKDEDDTPETC  443
               .:..:|||.: |: |.:... |.|. | .  .:  .:. . .:|| .|
NAF-1   230  LKALPPIARVTLVRL.RQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDC  278

rFSP    444  IYSNWSPWSACSSSTCEKGKRMRQRMLKAQ.LDLSVPCPDTQDGQPCMGP  492
               | ||.|: |:: ..  |.: | | ::.|  : : |||: :: ..|:..
NAF-1   279  EVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVPD  328

rFSP    493  GCSDEDGSTCTMSEWITWSPCSVSCGMGMRSRERYVKQFPEDGSVCMLPT  542
              .|
NAF-1   329  NCV.....................................................  331
```

FIG.2

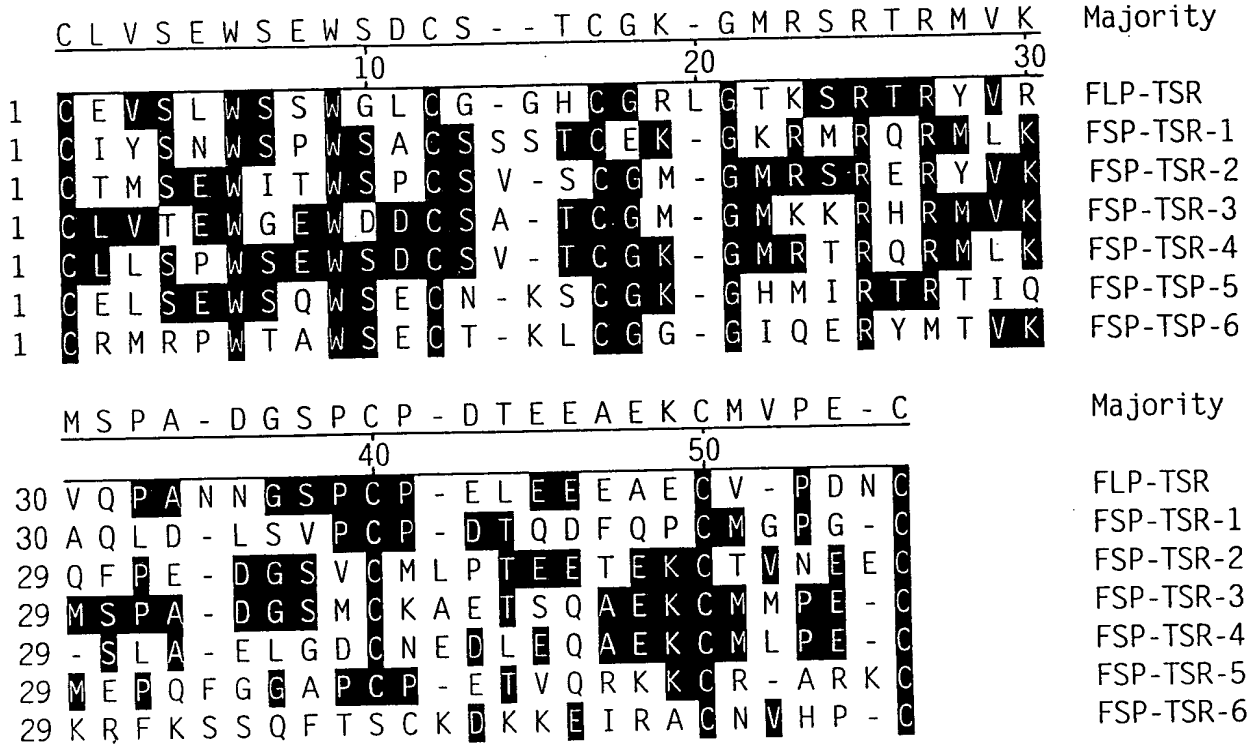
C L V S E W S E W S D C S - - T C G K - G M R S R T R M V K
Majority
10
20
30
1 C E V S L W S S W G L C G - G H C G R L G T K S R T R Y V R
FLP-TSR
1 C I Y S N W S P W S A C S S S T C E K - G K R M R Q R M L K
FSP-TSR-1
1 C T M S E W I T W S P C S V - S C G M - G M R S R E R Y V K
FSP-TSR-2
1 C L V T E W G E W D D C S A - T C G M - G M K K R H R M V K
FSP-TSR-3
1 C L L S P W S E W S D C S V - T C G K - G M R T R Q R M L K
FSP-TSP-4
1 C E L S E W S Q W S E C N - K S C G K - G H M I R T R T I Q
FSP-TSP-5
1 C R M R P W T A W S E C T - K L C G G - G I Q E R Y M T V K
FSP-TSP-6
M S P A - D G S P C P - D T E E A E K C M V P E - C
Majority
40
50
30 V Q P A N N G S P C P - E L E E E A E C V - P D N C
FLP-TSR
30 A Q L D - L S V P C P - D T Q D F Q P C M G P G - C
FSP-TSR-1
29 Q F P E - D G S V C M L P T E E T E K C T V N E E C
FSP-TSR-2
29 M S P A - D G S M C K A E T S Q A E K C M M P E - C
FSP-TSR-3
29 - S L A - E L G D C N E D L E Q A E K C M L P E - C
FSP-TSR-4
29 M E P Q F G G A P C P - E T V Q R K K C R - A R K C
FSP-TSR-5
29 K R F K S S Q F T S C K D K K E I R A C N V H P - C
FSP-TSR-6

FIG.3

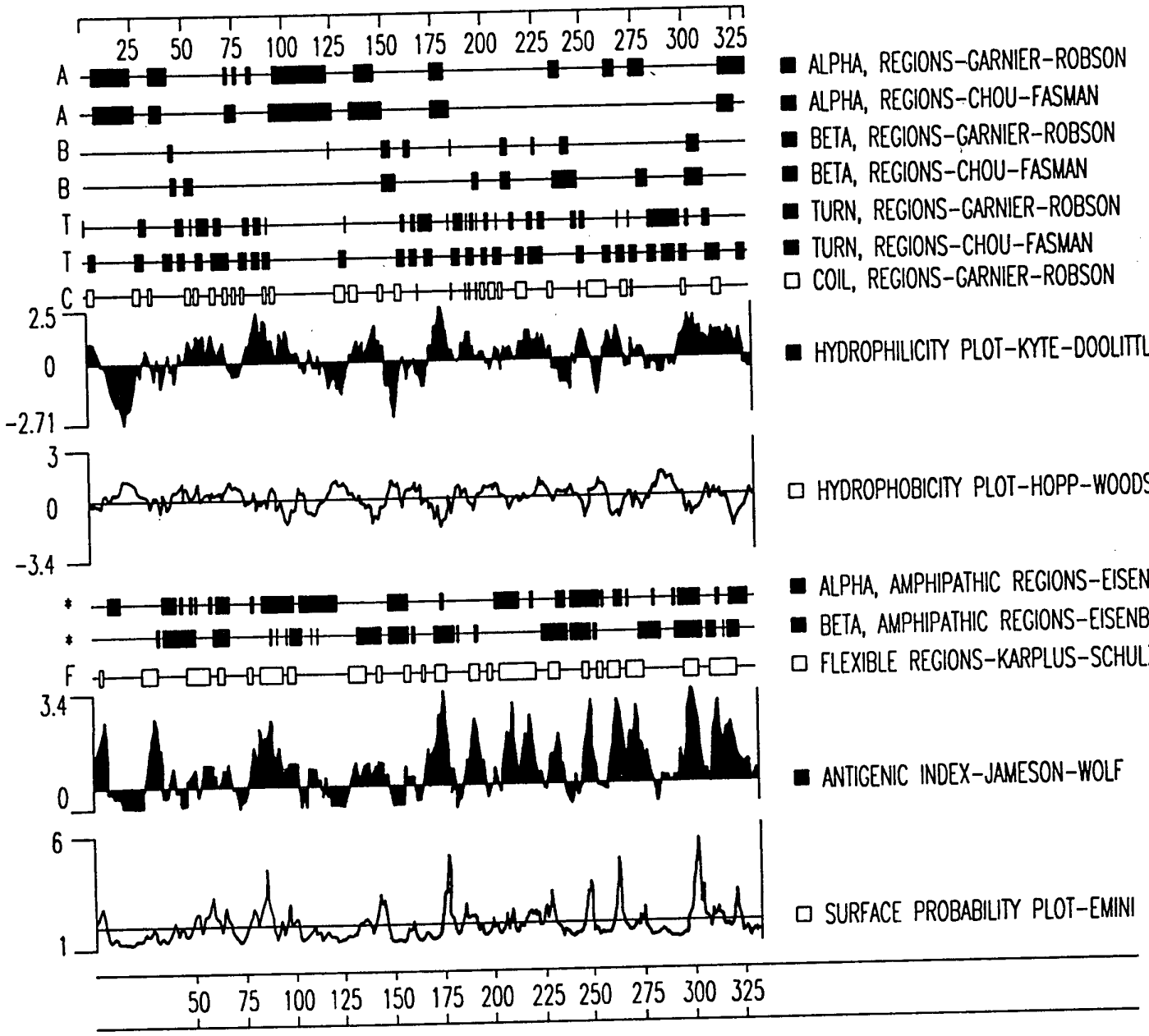

FIG.4